

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/043 787A
Source: IFW16
Date Processed by STIC: 11/14/2005

ENTERED



IFW/p

RAW SEQUENCE LISTING

DATE: 11/14/2005

PATENT APPLICATION: US/10/043,787A

TIME: 08:52:09

Input Set : D:\46699-20002.21 - SEQLIST.TXT

Output Set: N:\CRF4\11142005\J043787A.raw

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4 <110> APPLICANT: Yuan, Chong-Sheng
6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING HOMOCYSTEINE
8 <130> FILE REFERENCE: 46699-20002.21
10 <140> CURRENT APPLICATION NUMBER: 10/043,787A
11 <141> CURRENT FILING DATE: 2002-01-10
13 <150> PRIOR APPLICATION NUMBER: US 09/457,205
14 <151> PRIOR FILING DATE: 1999-12-06
16 <150> PRIOR APPLICATION NUMBER: US 09/347,878
17 <151> PRIOR FILING DATE: 1999-07-06
19 <150> PRIOR APPLICATION NUMBER: US 60/301,895
20 <151> PRIOR FILING DATE: 2001-06-29
22 <160> NUMBER OF SEQ ID NOS: 188
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 432
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
31 <400> SEQUENCE: 1
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33 1 5 10 15
34 Trp Gly Arg Lys Ala Leu Asp Ile Ala Glu Asn Glu Met Pro Gly Leu
35 20 25 30
36 Met Arg Met Arg Glu Arg Tyr Ser Ala Ser Lys Pro Leu Lys Gly Ala
37 35 40 45
38 Arg Ile Ala Gly Cys Leu His Met Thr Val Glu Thr Ala Val Leu Ile
39 50 55 60
40 Glu Thr Leu Val Thr Leu Gly Ala Glu Val Gln Trp Ser Ser Cys Asn
41 65 70 75 80
42 Ile Phe Ser Thr Gln Asn His Ala Ala Ala Ile Ala Lys Ala Gly
43 85 90 95
44 Ile Pro Val Tyr Ala Trp Lys Gly Glu Thr Asp Glu Glu Tyr Leu Trp
45 100 105 110
46 Cys Ile Glu Gln Thr Leu Tyr Phe Lys Asp Gly Pro Leu Asn Met Ile
47 115 120 125
48 Leu Asp Asp Gly Gly Asp Leu Thr Asn Leu Ile His Thr Lys Tyr Pro
49 130 135 140
50 Gln Leu Leu Pro Gly Ile Arg Gly Ile Ser Glu Glu Thr Thr Thr Gly
51 145 150 155 160
52 Val His Asn Leu Tyr Lys Met Met Ala Asn Gly Ile Leu Lys Val Pro
53 165 170 175
54 Ala Ile Asn Val Asn Asp Ser Val Thr Lys Ser Lys Phe Asp Asn Leu
55 180 185 190
56 Tyr Gly Cys Arg Glu Ser Leu Ile Asp Gly Ile Lys Arg Ala Thr Asp

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57          195          200          205
58 Val Met Ile Ala Gly Lys Val Ala Val Val Ala Gly Tyr Gly Asp Val
59          210          215          220
60 Gly Lys Gly Cys Ala Gln Ala Leu Arg Gly Phe Gly Ala Arg Val Ile
61 225          230          235          240
62 Ile Thr Glu Ile Asp Pro Ile Asn Ala Leu Gln Ala Ala Met Glu Gly
63          245          250          255
64 Tyr Glu Val Thr Thr Met Asp Glu Ala Cys Gln Glu Gly Asn Ile Phe
65          260          265          270
66 Val Thr Thr Thr Gly Cys Ile Asp Ile Ile Leu Gly Arg His Phe Glu
67          275          280          285
68 Gln Met Lys Asp Asp Ala Ile Val Cys Asn Ile Gly His Phe Asp Val
69          290          295          300
70 Glu Ile Asp Val Lys Trp Leu Asn Glu Asn Ala Val Glu Lys Val Asn
71 305          310          315          320
72 Ile Lys Pro Gln Val Asp Arg Tyr Arg Leu Lys Asn Gly Arg Arg Ile
73          325          330          335
74 Ile Leu Leu Ala Glu Gly Arg Leu Val Asn Leu Gly Cys Ala Met Gly
75          340          345          350
76 His Pro Ser Phe Val Met Ser Asn Ser Phe Thr Asn Gln Val Met Ala
77          355          360          365
78 Gln Ile Glu Leu Trp Thr His Pro Asp Lys Tyr Pro Val Gly Val His
79          370          375          380
80 Phe Leu Pro Lys Lys Leu Asp Glu Ala Val Ala Glu Ala His Leu Gly
81 385          390          395          400
82 Lys Leu Asn Val Lys Leu Thr Lys Leu Thr Glu Lys Gln Ala Gln Tyr
83          405          410          415
84 Leu Gly Met Ser Cys Asp Gly Pro Phe Lys Pro Asp His Tyr Arg Tyr
85          420          425          430
88 <210> SEQ ID NO: 2
89 <211> LENGTH: 2211
90 <212> TYPE: DNA
91 <213> ORGANISM: Homo sapiens
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95 tgccctacaa agtcgccgac atcggcctgg ctgcctgggg acgcaaggcc ctggacattg      120
96 ctgagaacga gatgccgggc ctgatcgta tgcgggagcg gtactcggcc tccaagccac      180
97 tgaaggcgcg cgcctcgt gctgcctgc acatgaccgt ggagacggcc gtcctcattg      240
98 agaccctcgt caccctgggt gctgaggtgc agtgggccag ctgcaacatc ttctccacc      300
99 agaaccatgc ggcggtgccc attgccaaagg ctggcattcc ggtgtatgcc tggaaggggc      360
100 aaacggacga ggagtacctg tgggtgcattg agcagaccct gtacttcaag gacggggccc      420
101 tcaacatgat tctggacgac gggggcgacc tcaccaacct catccacacc aagtaccgcg      480
102 agcttctgcc aggcattccga ggcattctctg aggagaccac gactgggggtc cacaacctct      540
103 acaagatgat ggccaatggg atcctcaagg tgcctgccat caatgtcaat gactccgtca      600
104 ccaagagcaa gtttgacaac ctctatggct gccgggagtc cctcatagat ggcattcaagc      660
105 gggccacaga tgtgatgatt gccggcaagg tagcggtggt agcaggctat ggtgatgtgg      720
106 gcaagggtctg tgcccaggcc ctgcgggggt tgcggagccc cgctcatcatc accgagattg      780
107 accccatcaa cgactgcag gctgccatgg agggctatga ggtgaccacc atggatgagg      840
108 cctgtcagga gggcaacatc tttgtcacca ccacaggctg tattgacatc atccttggcc      900

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109 ggtaggtgcc agatggggggg tcccggggag tgagggagga gggcagagtt gggacagctt      960
110 tctgtccctg acaatctccc acggtcttgg gctgcctgac aggcactttg agcagatgaa      1020
111 ggatgatgcc atttgtgtga acattggaca ctttgacgtg gagatcgatg tcaagtggct      1080
112 caacgagAAC gccgtggaga aggtgaacat caagccgcag gtggaccggg atcggttgaa      1140
113 gaatgggCGC cgcacatccc tgctggccga gggtcggctg gtcaacctgg gttgtgccat      1200
114 gggccacccc agcttcgtga tgagtaactc cttcaccaac caggtgatgg cgcagatcga      1260
115 gctgtggacc catccagaca agtaccctgt tggggttcat ttctgcccc agaagctgga      1320
116 tgaggcagtg gctgaagccc acctgggcaa gctgaatgtg aagttgacca agctaactga      1380
117 gaagcaagcc cagtacctgg gcatgtcctg tgatggcccc ttcaagccgg atcactaccg      1440
118 ctactgagag ccaggtctgc gtttcacctt ccagctgctg tccttgcccc ggccccacct      1500
119 ctctctcccta agagctaatt gcaccaactt tgtgattggg ttgtcagtgt ccccatcga      1560
120 ctctctgggg ctgatcactt agtttttggc ctctgctgca gccgtcatac tgttccaaat      1620
121 gtggcagcgg gaacagagta ccctcttcaa gccccgggca tgatggaggt cccagccaca      1680
122 gggaaccatg agctcagtgg tcttggaaaca gctcactaag tcagtccttc cttagcctgg      1740
123 aagtcagtag tggagtcaca aagcccatgt gttttgccat ctaggccttc acctggtctg      1800
124 tggacttata cctgtgtgct tggtttacag gtccagtggt tcttcagccc atgacagatg      1860
125 agaaggggct atattgaagg gcaaagagga actgttgttt gaattttcct gagagcctgg      1920
126 cttagtgtct ggccctctct taaacctcat tacaatgagg ttagtacttt tagtccctgt      1980
127 ttacagggg ttagaataga ctgttaaggg gcaactgaga aagaacagag aagtgacagc      2040
128 taggggttga gaggggccc aaaaacatga atgcaggcag atttcgtgaa atctgccacc      2100
129 actttataac cagatgggtc ctttcacaa cctgggtcaa aaagagaata atttggccta      2160
130 taatgttaaa agaaagcagg aaggtgggta aataaaaaatc ttggtgcctg g          2211
132 <210> SEQ ID NO: 3
133 <211> LENGTH: 2226
134 <212> TYPE: DNA
135 <213> ORGANISM: Homo sapiens
137 <220> FEATURE:
138 <221> NAME/KEY: misc_feature
139 <222> LOCATION: (1)...(2226)
140 <223> OTHER INFORMATION: n = A,T,C or G
142 <400> SEQUENCE: 3
143 gttgccagct tgcacatgcc atcatttgat gcccacctta cagagctgac agatgaccaa      60
144 gcaaaatata tgggactcaa caaaatggg ccattcaaac ctaattatta cagatactaa      120
145 tggaccatac taccaaggac cagtcacact gaaccacaca ctctaaagaa atatttttta      180
146 agataacttt tattttcttc ttactccttt cctcttgatt tttttcctat aatttcattc      240
147 ttgttttttc atctcattat ccaagttctg cagaccacac aggaacttgc ttcattggctc      300
148 tttagatgaa atagaagttc agggttcctc actctagtca ctaaagaagg attttactct      360
149 cccagcccag aaaggtgatt ctttctttac catttctggg gacttttagtc ttaattaggt      420
150 accttattaa caggaaatgc taaggtacct tctctgtgga acaatctgca atgtctaaat      480
151 cgccttaaaa gagcccattt cttagctgct gaaatcagtg ctctttcact tcttcagaga      540
152 agcagggatg gtacctaccc ggcaggtagg ttagatgtgg gtggtgcatg ttaatttccc      600
153 ttagaagttc caagccctgt ttctgctgta aaggtgggat gtccagttca gagatgtgta      660
154 taatgagcat ggcttgtaa gatcaggagg cccacttgga tttatagat agcccttcct      720
155 cactccac cagacttgct catttttcga gtttttaact agactacact ctattgagtt      780
-> 156 taattttgtc ctctaggatt tatttctggt gtccaaaaaa aaaanaaaag aaaagaaaaa      840
157 ttaaggagaa tttttgggtg taatgctgag gaattgcttg agtggttagt tgttaccaat      900
158 ttctcttttg aacctttgga gctaaggatg ctgagcttag agaaatgcta gtctcaagcc      960
159 ctgttaagtc cctctgtttc tagcccgtag ttcatacat cagtgaactg gagccacaac      1020
160 agcaaattct atcagctgtg taccatacag cttgtgctga aggcgaattt cttgagccat      1080

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161 tactcagtat aaagcactga gttctatctt taggatttat ctttaagagc aaatttctgg 1140
162 tcagctgtgc ttctgcaacc taaaatatatt aaaggagggt aggtgtgggc aggaggagga 1200
163 atgataaatt gggccagggc aagaaaaatc tagcttcata taatttgtct gggactatac 1260
164 accctatata atgttagttt tacagaagta atatgacttt tgattgctac ataccacaaa 1320
165 gagtttatga actgagatca taaagggcaa ctgatgtgtg aagaaagtag tcagtacatc 1380
166 ctggctcatg ctctgaaaga atatccagag aggcctctctc aaagatcagg gagatgtatt 1440
167 cccatgccat gcaccctgct tcccagcatt tctgcatggc caagtgagct ttatgctcat 1500
168 gagctttaag tatataatta tccaggattt taaatcctca acttgttcta gcttgtgatc 1560
169 cctcaaagtt gggctacacg ttagtgctag atactagaaa ttttcaactt tccactgatc 1620
170 agagagacag acattaaaaa caaaaataga agaaaggaaa gctttcacc c tgcagcttct 1680
171 tagcagggaa caattgtctt gccaaaactt ttttcccttt tctctcccat tttcttttac 1740
172 ccaatccctt cttactcctt gccagtgtga ccatgctttc ttctctgtag atgttaacag 1800
173 ttaaggccta ttttccctcg gcacttaacc aaccaatcag aacaccacat ctgtagggg 1860
174 aggtaacctg gccaacagtg tatccatcac gttagccctg ctggaggaggaa gggaccacaa 1920
175 ttcacctgcc ctctgacctg ccccttgatc ccatatctat taccgtgtcc ataggaataa 1980
176 taggtaaggg ctctgtctct gtcaagccat gtaacaaagg acactgttaa aaaaaaaaaa 2040
177 aagtctggca tcagaggagg catgtggaga gcaactggg aagaacaagt tcattttgta 2100
178 ttgaatgatt tttaatgaat gcaatattaa tccttgca tgagcaataa tcattaaaat 2160
-> 179 cgattaaaaat grtaagrcct taaaaaaaaa aaanaaggnn gagaaggang gnnnggggtg 2220
-> 180 nngngg 2226

182 <210> SEQ ID NO: 4
183 <211> LENGTH: 27
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Primer
190 <400> SEQUENCE: 4
191 ggccccttcg agccgatca ctaccgc 27
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 27
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
200 of human SAH hydrolases
202 <400> SEQUENCE: 5
203 gacttcgtca ccgagcga gtttggg 27
205 <210> SEQ ID NO: 6
206 <211> LENGTH: 27
207 <212> TYPE: DNA
208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
212 of human SAH hydrolases
214 <400> SEQUENCE: 6
215 cccaaacttg ctggcggtga cgaagtc 27
217 <210> SEQ ID NO: 7
218 <211> LENGTH: 27
219 <212> TYPE: DNA

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220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
224     of human SAH hydrolases
226 <400> SEQUENCE: 7
227 aacattggac actctgacgt ggagatc                                27
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231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
236     of human SAH hydrolases
238 <400> SEQUENCE: 8
239 gatctccacg tcagagtgtc caatgtt                                27
241 <210> SEQ ID NO: 9
242 <211> LENGTH: 27
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
248     of human SAH hydrolases
250 <400> SEQUENCE: 9
251 tgtaacattg gagactttga cgtggag                                27
253 <210> SEQ ID NO: 10
254 <211> LENGTH: 27
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
260     of human SAH hydrolases
262 <400> SEQUENCE: 10
263 ctccacgtca aagtctccaa tggtaca                                27
265 <210> SEQ ID NO: 11
266 <211> LENGTH: 27
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
272     of human SAH hydrolases
274 <400> SEQUENCE: 11
275 tgtgccatgg gctccccag cttegtg                                27
277 <210> SEQ ID NO: 12
278 <211> LENGTH: 27
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Oligonucleotide used for site-directed mutagenesis
284     of human SAH hydrolases

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Base Note:

Presence of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
<223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 825, 2194, 2199, 2200, 2209, 2212, 2213, 2221, 2222, 2224

VERIFICATION SUMMARY

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156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:780
179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2160
180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2220
172 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28